What is claimed is:

1. A method for detecting or quantifying a target nucleic acid in a sample comprising:

(a) preparing a primer complementary to a sequence immediately upstream of a target nucleotide base at a predetermined position in a template of a nucleic acid of interest;

(b) treating a sample containing the nucleic acid of interest, if the nucleic acid is double-stranded, so as to obtain unpaired nucleotide bases spanning the specific position, or directly employing step (c) if the nucleic acid of interest is single-stranded;

(c) annealing the primer from (a) with the target nucleic acid from (b) under high stringency conditions to obtain a primer-nucleic acid duplex, wherein the target nucleotide base in the nucleic acid of interest is the first unpaired base immediately downstream of the 3' end of the primer;

(d) mixing the primer-nucleic acid duplex from (c) with a primer extension reaction reagent comprising: (i) one type of terminator nucleotide or optionally, absence of a nucleotide, that is complementary to the target base at the predetermined position of the nucleic acid of interest, and (ii) three types of non-terminator nucleotides that are different from the terminator nucleotide in (i), and at least one type is optionally labeled with a detectable marker;

(e) performing the primer extension reaction by enzymatic or chemical means, wherein the incorporation of said terminator nucleotide or non-terminator nucleotide to the primer depends upon the identity of the unpaired nucleotide base in the nucleic acid template immediately downstream of the 3' end of the primer, and wherein incorporation of said terminator nucleotide in the sequence complementary to said target nucleotide base in the nucleic acid of interest will terminate said primer extension without incorporating any labeled non-terminator nucleotide into the primer, wherein said primer is not labeled, and further wherein, when the target nucleotide base is changed to any other type of nucleotide, one of the non-terminator nucleotides labeled with said detectable maker, or optionally not labeled with any marker if mass spectrometry is used

as a detecting method, that is complementary to the mutated nucleotide base, is sequence-dependently incorporated into the primer by said primer extension reaction; and

(f) determining the presence and identity of the nucleotide base at the predetermined position in the nucleic acid of interest by detecting the incorporated labeled non-terminator in the primer.

2. The method according to claim 1, wherein the primer is a fragment of deoxyribonucleic or ribonucleic acid, an oligodeoxyribonucleotide, an oligoribonucleotide, or a copolymer of deoxyribonucleic acid and ribonucleic acid.

3. The method according to claim 1, wherein the nucleic acid of interest is deoxyribonucleic acid, a ribonucleic acid, or a copolymer of deoxyribonucleic acid and ribonucleic acid.

4. The method according to claim 1, wherein the target nucleotide is defined as any known base, which include wild-type or a known mutant base so long as the base is known and it is desired to know its variant.

5. The method according to claim 1, wherein the terminator nucleotide is a dideoxyribonucleotide and the non-terminator nucleotide is a deoxyribonucleotide or a ribonucleotide.

6. The method according to claim 1, wherein the terminator nucleotide is unlabeled.

7. The method according to claim 1, wherein the terminator nucleotide is labeled with a detectable marker that is different from the marker on the non-terminators.

8. The method according to claim 1, wherein in step (d), the duplex from step (c) is contacted with non-terminator nucleotides, wherein each non-terminators is labeled with the same or different detectable marker.

9. The method according to claim 1, wherein said detectable marker comprises an enzyme, radioactive isotope, a fluorescent molecule, or a protein ligand.

10. The method according to claim 1, wherein said detecting is carried out by mass spectrometry.

11. The method according to claim 1, wherein said enzyme is template-dependent.

12. The method of claim 11, wherein the template-dependent enzyme is DNA polymerase.

13. The method according to claim 12, wherein the DNA polymerase is *E. coli* DNA polymerase I or the "Klenow fragment" thereof, T4 DNA polymerase, T7 DNA polymerase, or *T. aquaticus* DNA polymerase.

14. The method according to claim 11, wherein said enzyme is RNA polymerase or reverse transcriptase.

15. The method according to claim 1, wherein the primer comprises one or more moieties that permit affinity separation of the primer from the unincorporated reagent and/or the nucleic acid of interest.

16 The method according to claim 1, wherein the primer comprises one or more moieties that allows linking the primer to a solid surface.

17. The method according to claim 15, wherein the moieties comprises biotin or digitonin.

18. The method according to claim 16, wherein the moieties comprises biotin or digitonin.

19. The method according to claim 15, wherein the moieties comprises a DNA or RNA sequence that permits affinity separation of the primer from the unincorporated reagent and/or the nucleic acid of interest via base pairing to a complementary sequence present in a nucleic acid attached to a solid support.

20. The method according to claim 16, wherein the moieties comprises a DNA or RNA sequence that permits affinity separation of the primer from the unincorporated reagent and/or the nucleic acid of interest via base pairing to a complementary sequence present in a nucleic acid attached to a solid support.

21. The method according to claim 15, wherein the moieties comprises a DNA or RNA sequence that allows the primer to link to a solid support via base pairing to a complementary sequence present in solid surface.

22. The method according to claim 16, wherein the moieties comprises a DNA or RNA sequence that allows the primer to link to a solid support via base pairing to a complementary sequence present in solid surface.

23. The method according to claim 1, wherein the nucleic acid of interest has been synthesized enzymatically *in vivo*, *in vitro*, or synthesized non-enzymatically.

24. The method according to claim 1, wherein the nucleic acid of interest is synthesized by polymerase chain reaction.

25. The method according to claim 1, wherein the nucleic acid of interest comprises non-natural nucleotide analogs.

26. The method according to claim 25, wherein the non-natural nucleotide analogs comprise deoxyinosine or 7-deaza-2'-deoxyguanosine.

27. The method according to claim 1, wherein the sample comprises genomic DNA from an organism, RNA transcripts thereof, or cDNA prepared from RNA transcripts thereof.

28. The method according to claim 1, wherein the sample comprises extragenomic DNA from an organism, RNA transcripts thereof, or cDNA prepared from RNA transcripts thereof.

29. The method according to claim 27, wherein the organism is a plant, microorganism, bacteria, virus.

30. The method according to claim 28, wherein the organism is a plant, microorganism, bacteria, virus.

31. The method according to claim 27, wherein the organism is a vertebrate or invertebrate.

32. The method according to claim 28, wherein the organism is a vertebrate or invertebrate.

33. The method according to claim 27, wherein the organism is a mammal.

34. The method according to claim 28, wherein the organism is a mammal.

35. The method according to claim 27, wherein the organism is a human being.

36. The method according to claim 27, wherein the organism is a human being.